

057  
1130

OIIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/916,790

DATE: 11/28/2001  
 TIME: 12:08:50

Input Set : D:\38155-20027.txt  
 Output Set: N:\CRF3\11212001\I916790.raw

**ENTERED**

3 <110> APPLICANT: Meyers, Rachael  
 4 Kapeller-Libermann, Rosana  
 5 Silos-Santiago, Immaculada  
 7 <120> TITLE OF INVENTION: 18431 AND 32374, NOVEL HUMAN PROTEIN  
 8 KINASE FAMILY MEMBERS AND USES THEREFOR  
 11 <130> FILE REFERENCE: 381552002700  
 13 <140> CURRENT APPLICATION NUMBER: 09/916,790  
 14 <141> CURRENT FILING DATE: 2001-07-27  
 16 <150> PRIOR APPLICATION NUMBER: 60/221,543  
 17 <151> PRIOR FILING DATE: 2000-07-28  
 19 <160> NUMBER OF SEQ ID NOS: 37  
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 2893  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Homo sapiens  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (274)...(1314)  
 32 <221> NAME/KEY: misc\_feature  
 33 <222> LOCATION: (1)...(2893)  
 34 <223> OTHER INFORMATION: n = A,T,C or G  
 36 <400> SEQUENCE: 1  
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 38 gtcctttgac cttgcttggtg ggccgaagga ctgccccctg ggccctgggtc cggtgtgtgcc 120  
 39 ccctttctcac ttgaagacat gcaggccctg actctccgca cacttggccc gccagcgacg 180  
 40 tcacccaagc acctacgaaa ctagtcccg gagctgggca aaggcaccta cggaaggtt 240  
 41 gatctggttg tctacaaggg cacaggcaca aaa atg gca ctg aag ttt gtg aac 294  
 42 Met Ala Leu Lys Phe Val Asn  
 43 1 5  
 45 aag agc aaa acc aag ctg aag aac ttc cta cgg gag gtg agc atc acc 342  
 46 Lys Ser Lys Thr Lys Leu Lys Asn Phe Leu Arg Glu Val Ser Ile Thr  
 47 10 15 20  
 49 aac agc ctc tcc tcc agc ccc ttc atc atc aag gtc ttt gac gtg gtc 390  
 50 Asn Ser Leu Ser Ser Ser Pro Phe Ile Ile Lys Val Phe Asp Val Val  
 51 25 30 35  
 53 ttt gag aca gag gac tgc tac gtc ttt gcc cag gag tac gca cct gct 438  
 54 Phe Glu Thr Glu Asp Cys Tyr Val Phe Ala Gln Glu Tyr Ala Pro Ala  
 55 40 45 50 55  
 57 ggg gac ctg ttt gac atc atc cct ccc cag gtg ggg ctc cct gag gac 486  
 58 Gly Asp Leu Phe Asp Ile Ile Pro Pro Gln Val Gly Leu Pro Glu Asp  
 59 60 65 70  
 61 acg gtg aag cgc tgt gtg cag cag ctg ggc ctg gcg ctg gac ttc atg 534  
 62 Thr Val Lys Arg Cys Val Gln Gln Leu Gly Leu Ala Leu Asp Phe Met  
 63 75 80 85  
 65 cac ggg cgg cag ctg gtg cac cgc gac atc aag ccc gag aac gtg ctg 582  
 66 His Gly Arg Gln Leu Val His Arg Asp Ile Lys Pro Glu Asn Val Leu

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67	90	95	100	
69	ctg ttc gac cgc gag tgc cgc cgc gta aag ctg gcc gac ttc ggc atg	630		
70	Leu Phe Asp Arg Glu Cys Arg Arg Val Lys Leu Ala Asp Phe Gly Met			
71	105 110 115			
73	acg cgc cgc gtg ggc tgc cgc gtc aag cgc gtg agc ggc acc atc cct	678		
74	Thr Arg Arg Val Gly Cys Arg Val Lys Arg Val Ser Gly Thr Ile Pro			
75	120 125 130 135			
77	tac acg gcg cct gag gtg tgc cag gcg ggc cgc gcc gac ggg ctg gcg	726		
78	Tyr Thr Ala Pro Glu Val Cys Gln Ala Gly Arg Ala Asp Gly Leu Ala			
79	140 145 150			
81	gtg gac acg ggc gtg gac gtg tgg gcc ttc ggc gtg ctc atc ttc tgc	774		
82	Val Asp Thr Gly Val Asp Val Trp Ala Phe Gly Val Leu Ile Phe Cys			
83	155 160 165			
85	gtg ctc acc ggc aac ttc ccg tgg gag gcg gcg tcg ggc gcc gac gcc	822		
86	Val Leu Thr Gly Asn Phe Pro Trp Glu Ala Ala Ser Gly Ala Asp Ala			
87	170 175 180			
89	ttc ttc gag gag ttc gtg cgc tgg cag cgg ggc cgc ctg ccg ggg ctg	870		
90	Phe Phe Glu Glu Phe Val Arg Trp Gln Arg Gly Arg Leu Pro Gly Leu			
91	185 190 195			
93	cct tcg cag tgg cgc cgc ttc acc gag ccc gcg ctg cgc atg ttc cag	918		
94	Pro Ser Gln Trp Arg Arg Phe Thr Glu Pro Ala Leu Arg Met Phe Gln			
95	200 205 210 215			
97	cgc tta ctg gcc ctg gag ccc gag cgc cgc ggc cca gcc aag gag gtg	966		
98	Arg Leu Leu Ala Leu Glu Pro Glu Arg Arg Gly Pro Ala Lys Glu Val			
99	220 225 230			
101	ttc cgc ttc ctc aag cac gag ctc acg tcc gag ctg cgc cgc cgg ccc	1014		
102	Phe Arg Phe Leu Lys His Glu Leu Thr Ser Glu Leu Arg Arg Arg Pro			
103	235 240 245			
105	tcg cac cgc gcg cgc aag ccc ccc ggg gac cgc ccg ccc gcc gcc ggg	1062		
106	Ser His Arg Ala Arg Lys Pro Pro Gly Asp Arg Pro Pro Ala Ala Gly			
107	250 255 260			
109	cca ctg cgc ctc gag gcg cct ggg ccg ctc aag cgg acg gtg ctg acc	1110		
110	Pro Leu Arg Leu Glu Ala Pro Gly Pro Leu Lys Arg Thr Val Leu Thr			
111	265 270 275			
113	gag agc ggc agc ggc tcc cgg ccc gcg ccc ccc gcc gtc ggg tcg gtg	1158		
114	Glu Ser Gly Ser Gly Ser Arg Pro Ala Pro Pro Ala Val Gly Ser Val			
115	280 285 290 295			
117	ccc ttg ccc gtg ccg gtg ccg gtg cca gtg ccc gtg ccg gtg cct gtg	1206		
118	Pro Leu Pro Val Pro Val Pro Val Pro Val Pro Val Pro Val Pro Val			
119	300 305 310			
121	ccc gag ccc ggc cta gct ccc cag ggg ccc ccc ggc cgg acc gac ggc	1254		
122	Pro Glu Pro Gly Leu Ala Pro Gln Gly Pro Pro Gly Arg Thr Asp Gly			
123	315 320 325			
125	cgc gcg gac aag agc aaa ggg cag gtg gtg ctg gcc acg gcc atc gag	1302		
126	Arg Ala Asp Lys Ser Lys Gly Gln Val Val Leu Ala Thr Ala Ile Glu			
127	330 335 340			
129	atc tgc gtc tga gtcgctccg ccgcccctcgg acccggggagc agcccggggcc	1354		
130	Ile Cys Val *			
131	345			

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133 cgccccgagc cgggtgcccgg tgcggcggtg ggggaatggag ccacctcgcc gcggggcagg 1414
134 gggcgcgagc gtagactagg caggacgcgg cccggcacct ggtccgtccc cggcgggctg 1474
135 gtgagggggc caccaaagac ccctagcgcg gcctggtgag cgggggcttg gccagagga 1534
136 gccaaagccg acagaccgga gaattcggag gccaccacac aacacacaca cacacacata 1594
137 cacacacaca cacacacacg ccaggagcaa gggagctttc gggccacact cccagacgcc 1654
138 tccctgagcc ctggaacccg gactcgttgc tcttgccctt ccataccccc tggcagatca 1714
139 tctgcggtc ccaccccaga tccccctctc ctgccatcc cattctgccc cctccccacc 1774
140 ctgggtacag aaagggactg aagtgttggg cagagagggg gcttaaggcc cctgggcaca 1834
141 ggctgggatc agggcagtga gcgaagggca gctgtgtcct gcccttcctt ctggaggctg 1894
142 gaggggagag gccaaagccct tggaaaatgt agcaaatgtc tggrrwkgctg cataagtgcg 1954
143 tgtatgtgcg ggacaggccc cgagaagcta gtgactcctg cacaccccca ttgcacaaat 2014
144 gaaatcacag cccaggaggg agggtagctt ggcactggct gagaaataga gctctctccc 2074
145 cgccccctcc cctaaccaca agggattgtc ctgacaactt gtggggatag aagggtcac 2134
146 agggcagggg tctcagctgc ccccatcctt agggcagggg agttagtgtg gagccgagag 2194
147 caggtcccg cccccctgc cagccgcact gtcccaggcc cagggaacct tgccgggtcc 2254
148 tcccagccct tgccacacag cctagacgta gtgactggg cttccagcag gtggcgagct 2314
149 ggttcgtgct ggaaatttct cctgggttct ttgggggtcaa acatgccaac ctccaagacc 2374
150 ccatacctcac gtctccact tttctggcgc tggagtgtgc agggcgtagg acctgcatgt 2434
151 gtgggtgtga gaatgggggc cgggtggacac cagggggcga gtgtgtgact aggtgtgtgt 2494
W--> 152 gcacatgtgt aggggtgcaga cgcattgggtg ccataccttg cnttcaatga ctgtgcgtcc 2554
W--> 153 agaccccaaa aaagcggccc ccccaccaca ccctgntcct cccaggcagc tgtcccaggg 2614
154 cgcccaggcc tgccttgca cacagccctc aggaatccg gcaaggaggc ccctgcaggt 2674
W--> 155 tggttcangc ccaggtagca aaacagagac aacagcagcc ccgcctgacc ccctgcccct 2734
W--> 156 ntctgtggag gccggggacc cccgcaataa gcaccacatg ggtgaggctg tccctgtcag 2794
W--> 157 ggnccctgc cagggtccct cctgggggtc tgggccattt gaggggctct ttgatgggcc 2854
W--> 158 aggcngcca gagtgaactc cgagcacttt ctggctggt 2893
160 <210> SEQ ID NO: 2
161 <211> LENGTH: 346
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 2
166 Met Ala Leu Lys Phe Val Asn Lys Ser Lys Thr Lys Leu Lys Asn Phe
167 1 5 10 15
168 Leu Arg Glu Val Ser Ile Thr Asn Ser Leu Ser Ser Ser Pro Phe Ile
169 20 25 30
170 Ile Lys Val Phe Asp Val Val Phe Glu Thr Glu Asp Cys Tyr Val Phe
171 35 40 45
172 Ala Gln Glu Tyr Ala Pro Ala Gly Asp Leu Phe Asp Ile Ile Pro Pro
173 50 55 60
174 Gln Val Gly Leu Pro Glu Asp Thr Val Lys Arg Cys Val Gln Gln Leu
175 65 70 75 80
176 Gly Leu Ala Leu Asp Phe Met His Gly Arg Gln Leu Val His Arg Asp
177 85 90 95
178 Ile Lys Pro Glu Asn Val Leu Leu Phe Asp Arg Glu Cys Arg Arg Val
179 100 105 110
180 Lys Leu Ala Asp Phe Gly Met Thr Arg Arg Val Gly Cys Arg Val Lys
181 115 120 125
182 Arg Val Ser Gly Thr Ile Pro Tyr Thr Ala Pro Glu Val Cys Gln Ala
183 130 135 140

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184 Gly Arg Ala Asp Gly Leu Ala Val Asp Thr Gly Val Asp Val Trp Ala
185 145 150 155 160
186 Phe Gly Val Leu Ile Phe Cys Val Leu Thr Gly Asn Phe Pro Trp Glu
187 165 170 175
188 Ala Ala Ser Gly Ala Asp Ala Phe Phe Glu Glu Phe Val Arg Trp Gln
189 180 185 190
190 Arg Gly Arg Leu Pro Gly Leu Pro Ser Gln Trp Arg Arg Phe Thr Glu
191 195 200 205
192 Pro Ala Leu Arg Met Phe Gln Arg Leu Leu Ala Leu Glu Pro Glu Arg
193 210 215 220
194 Arg Gly Pro Ala Lys Glu Val Phe Arg Phe Leu Lys His Glu Leu Thr
195 225 230 235 240
196 Ser Glu Leu Arg Arg Arg Pro Ser His Arg Ala Arg Lys Pro Pro Gly
197 245 250 255
198 Asp Arg Pro Pro Ala Ala Gly Pro Leu Arg Leu Glu Ala Pro Gly Pro
199 260 265 270
200 Leu Lys Arg Thr Val Leu Thr Glu Ser Gly Ser Gly Ser Arg Pro Ala
201 275 280 285
202 Pro Pro Ala Val Gly Ser Val Pro Leu Pro Val Pro Val Pro Val Pro
203 290 295 300
204 Val Pro Val Pro Val Pro Val Pro Glu Pro Gly Leu Ala Pro Gln Gly
205 305 310 315 320
206 Pro Pro Gly Arg Thr Asp Gly Arg Ala Asp Lys Ser Lys Gly Gln Val
207 325 330 335
208 Val Leu Ala Thr Ala Ile Glu Ile Cys Val
209 340 345
211 <210> SEQ ID NO: 3
212 <211> LENGTH: 1041
213 <212> TYPE: DNA
214 <213> ORGANISM: Homo sapiens
216 <400> SEQUENCE: 3
217 atggcactga agtttgtgaa caagagcaaa accaagctga agaacttcct acgggaggtg 60
218 agcatcacca acagcctctc ctccagcccc ttcatcatca aggtctttga cgtggtcttt 120
219 gagacagagg actgctacgt ctttgcccag gagtacgcac ctgctgggga cctgtttgac 180
220 atcatccctc cccaggtggg gctccctgag gacacgggtg agcgtctgtg gcagcagctg 240
221 ggcttgccgc tggacttcat gcacggggcg cagctggtgc accgcgacat caagcccag 300
222 aacgtgctgc tgttcgaccg cgagtgcgcg cgcgtaaagc tggccgactt cggcatgacg 360
223 cgcgcgctgg gctgccgcgt caagcgcgtg agcggcacca tcccttacac ggcgcctgag 420
224 gtgtgccagg cgggcccgcg cgacgggctg gcggtggaca cgggcgtgga cgtgtgggcc 480
225 ttcggcgtgc tcatcttctg cgtgctcacc ggcaacttcc cgtgggaggg ggcgtcgggc 540
226 gccgacgcct tcttcgagga gttcgtgccc tggcagcggg gccgcctgcc ggggctgcct 600
227 tcgcagtggc gccgcttcac cgagcccgcg ctgcgcattg tccagcgtt actggccctg 660
228 gagcccagag gccgcggccc agccaaggag gtgttccgct tctcaagca cgagctcacg 720
229 tccgagctgc gccgcggccc ctgcacccgc gcgcgcaagc cccccgggga ccgcccgcc 780
230 gccgccgggc cactgcgcct cgaggcgctt gggccgctca agcggacggg gctgaccgag 840
231 agcggcagcg gctcccggcc cgcgcgcgcc gccgtcgggt cgggtgccctt gccctgccc 900
232 gtgcccgtgc cagtgcgcgt gccggtgcct gtgcccagc cgggcctagc tccccgggg 960
233 cccccggcc ggaccgacgg ccgcgcggac aagagcaaag ggcaggtggg gctggccacg 1020
234 gccatcgaga tctgcgtctg a 1041

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236 <210> SEQ ID NO: 4
237 <211> LENGTH: 4136
238 <212> TYPE: DNA
239 <213> ORGANISM: Homo sapiens
241 <220> FEATURE:
242 <221> NAME/KEY: CDS
243 <222> LOCATION: (551)...(3233)
245 <400> SEQUENCE: 4
246 cttcctcttc ctgtgtctcag tcccattaac ctgccataacc acggctcctc gtcttcccaa      60
247 ttccttcacc cagtattttc aatcgacccc ccccgctccc cccgcacctc tttctctctc      120
248 gctatatgtc ctttctgtggc cagtttgggc aaggggaagg acaccacaag tcgggggtctt      180
249 tcctcagcgt tgggtcgcgg tggtctgtgag ggcggaagaa aaggccaggc tgaggggagg      240
250 gtagaggggtg aaaagctcgg atctgtgttt ggggaaggcc aggcttgccg tcctcgccgg      300
251 gttccgcgaa ggtaacctt ggctgacttg gctcgcgagc aaagggcagc gtctgagctc      360
252 ccggcgttcc aggagtggcc tttttttag gagcacctga aatgcagcgt ctggtgact      420
253 aagccgtagc ggcagcagca gccacagcga cagcgtggg gccctgtgta gaagctccat      480
254 ccccttgtc tttgtgcttg cctgcgtccc cagactcaga gattatctta gaagacctag      540
255 gactccaaaa atg ttt ccc ctg aag gac gct gaa atg gga gcc ttt acc      589
256           Met Phe Pro Leu Lys Asp Ala Glu Met Gly Ala Phe Thr
257           1           5           10
259 ttc ttt gcc tcg gct ctg cca cat gat gtt tgt gga agc aat gga ctt      637
260 Phe Phe Ala Ser Ala Leu Pro His Asp Val Cys Gly Ser Asn Gly Leu
261           15           20           25
263 cct ctc aca cca aat tcc atc aaa att tta ggg cgc ttt caa atc ctt      685
264 Pro Leu Thr Pro Asn Ser Ile Lys Ile Leu Gly Arg Phe Gln Ile Leu
265           30           35           40           45
267 aaa acc atc acc cat ccc aga ctc tgc cag tat gtg gat att tct agg      733
268 Lys Thr Ile Thr His Pro Arg Leu Cys Gln Tyr Val Asp Ile Ser Arg
269           50           55           60
271 gga aag cat gaa cga cta gtg gtc gtg gct gaa cat tgt gaa cgt agt      781
272 Gly Lys His Glu Arg Leu Val Val Val Ala Glu His Cys Glu Arg Ser
273           65           70           75
275 ctg gaa gac ttg ctt cga gaa agg aaa cct gtg agc tgt tca acg gtt      829
276 Leu Glu Asp Leu Leu Arg Glu Arg Lys Pro Val Ser Cys Ser Thr Val
277           80           85           90
279 ttg tgt ata gca ttt gag gtt ctt cag ggc ttg cag tat atg aac aaa      877
280 Leu Cys Ile Ala Phe Glu Val Leu Gln Gly Leu Gln Tyr Met Asn Lys
281           95           100           105
283 cat ggt ata gta cac agg gca ttg tct cct cat aat atc ctg ttg gac      925
284 His Gly Ile Val His Arg Ala Leu Ser Pro His Asn Ile Leu Leu Asp
285           110           115           120           125
287 cga aag gga cat att aaa ttg gct aaa ttt gga ctt tat cac atg aca      973
288 Arg Lys Gly His Ile Lys Leu Ala Lys Phe Gly Leu Tyr His Met Thr
289           130           135           140
291 gct cat ggt gat gat gtt gat ttc cca ata ggg tat ccc tcg tac ttg      1021
292 Ala His Gly Asp Asp Val Asp Phe Pro Ile Gly Tyr Pro Ser Tyr Leu
293           145           150           155
295 gcc cct gag gta att gca cag gga att ttc aaa acc act gat cac atg      1069
296 Ala Pro Glu Val Ile Ala Gln Gly Ile Phe Lys Thr Thr Asp His Met

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/916,790

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Input Set : D:\38155-20027.txt

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L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:483 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:1481 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1483 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1491 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:1513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37